



SEQUENCE LISTING

<110> Turner, Alex
Zambrowicz, Brian
Nehls, Michael
Freidrich, Glenn A.
Sands, Arthur T.

<120> A NOVEL HUMAN cDNA CLONE AND PROTEINS
ENCODED THEREBY

<130> 8535-0036-999

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1116

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(1113)

<400> 1

atg gga cat aaa gtg gtt gtc ttc gac att tct gtc atc aga gcc ttg	48
Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu	
1 5 10 15	
tg gaa act cgt gtc aag aag cac aaa gct tgg cag aag aag gag gtg	96
Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val	
20 25 30	
gaa agg ctt gag aag agc gcc ttg gag aag ata aag gag gag tgg aac	144
Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Glu Trp Asn	
35 40 45	
ttt gtg gcc gaa tgc agg agg aag ggc atc ccc cag gct gta tac tgc	192
Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys	
50 55 60	
aag aat ggc ttc ata gac acc agc gtg cgg ctt ctg gac aag att gaa	240
Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu	
65 70 75 80	
agg aac act ctc aca agg cag agt tca ctt ccc aag gac aga ggc aaa	288
Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys	
85 90 95	
cgg agc agt gcg ttt gtg ttt gaa ctt tct ggg gag cac tgg acg gag	336
Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu	
100 105 110	
ctc cca gat tca ttg aag gag cag aca cac ctg aga gaa tgg tac ata	384
Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile	
115 120 125	
agc aat acc ttg att caa atc att cct aca tat att cag tta ttt caa	432
Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln	
130 135 140	

gcg atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro 145 150 155 160	480
gca gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe 165 170 175	528
aac tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu 180 185 190	576
gag aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe 195 200 205	624
gaa tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn 210 215 220	672
aag ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln 225 230 235 240	720
tgg ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile 245 250 255	768
gac agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu 260 265 270	816
acc tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu 275 280 285	864
gtc gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp 290 295 300	912
tca tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp 305 310 315 320	960
aat gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp 325 330 335	1008
cgc caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu 340 345 350	1056
aaa gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser 355 360 365	1104
ctt caa ctt tga Leu Gln Leu 370	1116

<210> 2

<211> 371
 <212> PRT
 <213> Homo sapien

<400> 2
 Met Gly His Lys Val Val Val Phe Asp Ile Ser Val Ile Arg Ala Leu
 1 5 10 15
 Trp Glu Thr Arg Val Lys Lys His Lys Ala Trp Gln Lys Lys Glu Val
 20 25 30
 Glu Arg Leu Glu Lys Ser Ala Leu Glu Lys Ile Lys Glu Trp Asn
 35 40 45
 Phe Val Ala Glu Cys Arg Arg Lys Gly Ile Pro Gln Ala Val Tyr Cys
 50 55 60
 Lys Asn Gly Phe Ile Asp Thr Ser Val Arg Leu Leu Asp Lys Ile Glu
 65 70 75 80
 Arg Asn Thr Leu Thr Arg Gln Ser Ser Leu Pro Lys Asp Arg Gly Lys
 85 90 95
 Arg Ser Ser Ala Phe Val Phe Glu Leu Ser Gly Glu His Trp Thr Glu
 100 105 110
 Leu Pro Asp Ser Leu Lys Glu Gln Thr His Leu Arg Glu Trp Tyr Ile
 115 120 125
 Ser Asn Thr Leu Ile Gln Ile Ile Pro Thr Tyr Ile Gln Leu Phe Gln
 130 135 140
 Ala Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro
 145 150 155 160
 Ala Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe
 165 170 175
 Asn Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu
 180 185 190
 Glu Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe
 195 200 205
 Glu Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn
 210 215 220
 Lys Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln
 225 230 235 240
 Trp Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile
 245 250 255
 Asp Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu
 260 265 270
 Thr Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu
 275 280 285
 Val Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp
 290 295 300
 Ser Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp
 305 310 315 320
 Asn Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp
 325 330 335
 Arg Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu
 340 345 350
 Lys Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser
 355 360 365
 Leu Gln Leu
 370

<210> 3
 <211> 681
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(678)

<400> 3

atg aga att ctg gat ctg cca aaa aac caa atc tca cat ctt cca gca	48
Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala	
1 5 10 15	
gaa atc ggt tgt ttg aag aac ctg aaa gaa ctc aat gtg ggt ttc aac	96
Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn	
20 25 30	
tat ctg aag agc att cct cca gaa ttg gga gat tgt gaa aat cta gag	144
Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu	
35 40 45	
aga ctg gat tgt tct gga aat cta gaa tta atg gag ctg ccc ttt gaa	192
Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu	
50 55 60	
tta agt aat ttg aag caa gtt aca ttt gta gat atc tca gca aac aag	240
Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys	
65 70 75 80	
ttt tcc agt gtc cca atc tgt gtc ctg cgg atg tcg aat ttg cag tgg	288
Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp	
85 90 95	
ttg gat atc agc agc aat aac ctg acc gac ctg ccg caa gat ata gac	336
Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp	
100 105 110	
agg cta gag gag ctg cag agc ttt ctc ttg tat aaa aac aag ttg acc	384
Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr	
115 120 125	
tac ctt ccc tat tcc atg ctg aac ctg aag aag ctc act ctg tta gtc	432
Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val	
130 135 140	
gtc agt ggg gac cat ttg gtg gag ctc cca act gcc ctt tgt gac tca	480
Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser	
145 150 155 160	
tcc aca cct tta aaa ttt gta agc ctt atg gac aat cct att gat aat	528
Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn	
165 170 175	
gcc caa tgt gaa gat ggc aat gaa ata atg gaa agt gaa cgg gat cgc	576
Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg	
180 185 190	
caa cat ttt gat aaa gaa gtt atg aaa gcc tat att gaa gac ctt aaa	624
Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys	
195 200 205	
gaa aga gaa tct gtt ccc agc tat acc acc aaa gtg tct ttt agc ctt	672
Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu	
210 215 220	
caa ctt tga	681
Gln Leu	
225	

<210> 4

<211> 226
 <212> PRT
 <213> Homo sapien

<400> 4
 Met Arg Ile Leu Asp Leu Pro Lys Asn Gln Ile Ser His Leu Pro Ala
 1 5 10 15
 Glu Ile Gly Cys Leu Lys Asn Leu Lys Glu Leu Asn Val Gly Phe Asn
 20 25 30
 Tyr Leu Lys Ser Ile Pro Pro Glu Leu Gly Asp Cys Glu Asn Leu Glu
 35 40 45
 Arg Leu Asp Cys Ser Gly Asn Leu Glu Leu Met Glu Leu Pro Phe Glu
 50 55 60
 Leu Ser Asn Leu Lys Gln Val Thr Phe Val Asp Ile Ser Ala Asn Lys
 65 70 75 80
 Phe Ser Ser Val Pro Ile Cys Val Leu Arg Met Ser Asn Leu Gln Trp
 85 90 95
 Leu Asp Ile Ser Ser Asn Asn Leu Thr Asp Leu Pro Gln Asp Ile Asp
 100 105 110
 Arg Leu Glu Glu Leu Gln Ser Phe Leu Leu Tyr Lys Asn Lys Leu Thr
 115 120 125
 Tyr Leu Pro Tyr Ser Met Leu Asn Leu Lys Lys Leu Thr Leu Leu Val
 130 135 140
 Val Ser Gly Asp His Leu Val Glu Leu Pro Thr Ala Leu Cys Asp Ser
 145 150 155 160
 Ser Thr Pro Leu Lys Phe Val Ser Leu Met Asp Asn Pro Ile Asp Asn
 165 170 175
 Ala Gln Cys Glu Asp Gly Asn Glu Ile Met Glu Ser Glu Arg Asp Arg
 180 185 190
 Gln His Phe Asp Lys Glu Val Met Lys Ala Tyr Ile Glu Asp Leu Lys
 195 200 205
 Glu Arg Glu Ser Val Pro Ser Tyr Thr Thr Lys Val Ser Phe Ser Leu
 210 215 220
 Gln Leu
 225